

SEQUENCE LISTING

<110> Braun, Ralph P.
Thomsen, Lindy
Van-Wely, Catherine
Ertl, Peter

<120> Adjuvant

<130> 033267-015

<140> US 10/102,622

<141> 2002-03-19

<160> 12

<170> FastSEQ for Windows Version 4.0

<210> 1

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<212> PRT

<213> Artificial Sequence

<220>

<223> HBsAg in BALB/C mice

<400> 1

Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu
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<210> 2

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> HSV CD8 in BALB/C mice

<400> 2

His Gly Pro Ser Leu Tyr Arg Thr Phe
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<210> 3

<211> 1503

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of the p55 gag insert in
pGagOptprpr2

<400> 3

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cttgaacggt ttgccgtcaa cccaggcctg ctggaaacat ctgagggatg tcgccagatc 180
ctggggcaat tgcagccatc cctccagacc gggagtgaag agctgaggtc cttgtataac 240

acagtggcta ccctctactg cgtacaccag aggatcgaga ttaaggatac caaggaggcc 300
 ttggacaaaa ttgaggagga gcaaaacaag agcaagaaga aggcccagca ggcagctgct 360
 gacactgggc atagcaacca ggtatcacag aactatccta ttgtccaaaa cattcaggc 420
 cagatggttc atcagccat cagccccccgg acgctcaatg cctgggtgaa gtttgcgaa 480
 gagaaggcct tttctcctga gtttatcccc atgttctccg ctttgagtga gggggccact 540
 cctcaggacc tcaatacatc gcttaataacc gtggcggcc atcaggccgc catgcaaatg 600
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 ggc当地atcg cgccccggaca gatgcgggag cctcgccgct ctgacattgc cgccaccacc 720
 tctacactgc aagagcaat cggatggatg accaacaatc ctcccatccc agttggagaa 780
 atctataaac ggtggatcat tctcggtctc aataaaaatig ttagaatgtta ctctccgaca 840
 tccatcttgc acattagaca gggacccaaa gacgctttta gggattacgt cgaccgggtt 900
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 gccaccctgg aagagatgt gacccgcgtc caggagtag gcggaaccgg acacaaagcc 1080
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 accgcccgcgca actgtcgggc cccttaggaag aaaggggtt ggaagtgcgg caaggaggg 1260
 caccagatga aagactgtac agaacgacag gccaatttc ttggaaagat ttggccgagc 1320
 tacaagggga gacctggtaa tttctcgcaaa agcaggcccg agcccaccgc ccccccgtgag 1380
 gaatccttca ggtccggagt ggagaccaca acgcctcccc aaaaacagga accaatcgac 1440
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 taa 1503

<210> 4

<211> 500

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acid sequence of p55 gag insert in
pGag0ptrpr2

<400> 4

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															20
His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu	Arg	Phe	Ala	Val	Asn	Pro
															35
Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg	Gln	Ile	Leu	Gly	Gln	Leu
															50
Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu	Leu	Arg	Ser	Leu	Tyr	Asn
															65
Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln	Arg	Ile	Glu	Ile	Lys	Asp
															85
Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu	Glu	Gln	Asn	Lys	Ser	Lys
															100
Lys	Lys	Ala	Gln	Gln	Ala	Ala	Asp	Thr	Gly	His	Ser	Asn	Gln	Val	
															115
Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile	Gln	Gly	Gln	Met	Val	His
															130
Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val	Glu	
															145
Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Ser	Ala	Leu	Ser
															165
Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr	Val	Gly
															180
Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys	Glu	Thr	Ile	Asn	Glu	Glu
															195
															200
															205

Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala
 210 215 220
 Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr
 225 230 235 240
 Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile
 245 250 255
 Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys
 260 265 270
 Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly
 275 280 285
 Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
 290 295 300
 Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr
 305 310 315 320
 Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala
 325 330 335
 Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly
 340 345 350
 Val Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser
 355 360 365
 Gln Val Thr Asn Ser Ala Thr Ile Met Met Gln Arg Gly Asn Phe Arg
 370 375 380
 Asn Gln Arg Lys Ile Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His
 385 390 395 400
 Thr Ala Arg Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys
 405 410 415
 Gly Lys Glu Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn
 420 425 430
 Phe Leu Gly Lys Ile Trp Pro Ser Tyr Lys Gly Arg Pro Gly Asn Phe
 435 440 445
 Leu Gln Ser Arg Pro Glu Pro Thr Ala Pro Pro Glu Glu Ser Phe Arg
 450 455 460
 Ser Gly Val Glu Thr Thr Pro Pro Gln Lys Gln Glu Pro Ile Asp
 465 470 475 480
 Lys Glu Leu Tyr Pro Leu Thr Ser Leu Arg Ser Leu Phe Gly Asn Asp
 485 490 495
 Pro Ser Ser Gln
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<210> 5

<211> 1515

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of the p17/24trNEF insert in
p17/24trNEF1

<400> 5

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ctagaacat tcgcagttaa tcctggctg ttagaaacat cagaaggctg tagacaaata 180
ctggacagc tacaaccatc ccttcagaca ggatcagaag aacttagatc attatataat 240
acatgtcaaa ccctctattt tttgtcatcaa aggatagaga taaaagacac caaggaagct 300
ttagacaaga tagaggaaga gcaaaacaaa agtaaaaaa aagcacacca agcagcagct 360
gacacaggac acagcaatca ggtcagccaa aattacccta tagtgcagaa catccagggg 420
caaatggtaatc atcaggccat atcacctaga actttaaatg catggtaaa agtagtagaa 480
gagaaggctt tcagcccaga agtgataccc atgtttcag cattatcaga aggagccacc 540

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ccacaagatt taaacaccat gctaaacaca gtgggggac atcaagcgc catgcaaatg 600
 ttaaaagaga ccatcaatga ggaagctgca gaatggata gagtgcattc agtgcattgca 660
 gggcttattg caccaggcca gatgagagaa ccaagggaa gtgacatagc aggaactact 720
 agtacccttc aggaacaaat aggatggatg acaaataatc cacctatccc agtaggagaa 780
 attataaaa gatggataat cctgggatta aataaaatag taagaatgt tagccctacc 840
 agcattctgg acataagaca aggacaaaaa gaaccctta gagactatgt agaccggttc 900
 tataaaactc taagagccga gcaagcttca caggaggtaa aaaattgttat gacagaaaacc 960
 ttgttggtcc aaaatgcgaa cccagattt aagactattt taaaagcatt ggjgaccagcg 1020
 gctacactag aagaaatgt gacagcatgt cagggagtag gaggaccgg ccataaggca 1080
 agagttttgg tgggtttcc agtcacaccc caggtacctt taagaccaat gacttacaag 1140
 gcagctgtat atcttagcca ctttttaaa gaaaaggggg gacttggagg gctaattcac 1200
 tcccaaagaa gacaagatat ccttgatctg tggatctacc acacacaagg ctacttccct 1260
 gattggcaga actacacacc agggccaggg gtcagatatc cactgacott tggatggtgc 1320
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 agcttggttac accctgttag cctgcatggg atggatgacc cgagagagaga agtgttagag 1440
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<210> 6

<211> 504

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acid sequence of the p17/24trNEF insert in
p17/24trNEF1

<400> 6

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Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys	Lys	Lys	Tyr	Lys	Lys	
									20			25		30	
His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu	Arg	Phe	Ala	Val	Asn	Pro
							35		40		45				
Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg	Gln	Ile	Leu	Gly	Gln	Leu
							50		55		60				
Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu	Leu	Arg	Ser	Leu	Tyr	Asn
							65		70		75			80	
Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln	Arg	Ile	Glu	Ile	Lys	Asp
							85		90				95		
Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu	Gln	Asn	Lys	Ser	Lys	
							100		105			110			
Lys	Lys	Ala	Gln	Gln	Ala	Ala	Asp	Thr	Gly	His	Ser	Asn	Gln	Val	
							115		120			125			
Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile	Gln	Gly	Gln	Met	Val	His
							130		135			140			
Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val	Val	Glu
							145		150			155			160
Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Ser	Ala	Leu	Ser
							165		170			175			
Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr	Val	Gly
							180		185			190			
Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys	Glu	Thr	Ile	Asn	Glu	Glu
							195		200			205			
Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val	His	Ala	Gly	Pro	Ile	Ala
							210		215			220			
Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser	Asp	Ile	Ala	Gly	Thr	Thr
							225		230			235			240
Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met	Thr	Asn	Asn	Pro	Pro	Ile

245	250	255
Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly	Lys	
260	265	270
Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp	Ile Arg Gln Gly	
275	280	285
Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe	Tyr Lys Thr Leu	
290	295	300
Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp	Met Thr Glu Thr	
305	310	315
Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr	Ile Leu Lys Ala	
325	330	335
Leu Gly Pro Ala Ala Thr Leu Glu Met Met Thr Ala	Cys Gln Gly	
340	345	350
Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Val	Gly Phe Pro Val	
355	360	365
Thr Pro Gln Val Pro Leu Arg Pro Met Thr Tyr	Lys Ala Ala Val Asp	
370	375	380
Leu Ser His Phe Leu Lys Glu Lys Gly Gly	Leu Glu Gly Leu Ile His	
385	390	395
Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu Trp	Ile Tyr His Thr Gln	
405	410	415
Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr Pro Gly	Pro Gly Val Arg	
420	425	430
Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys Leu Val	Pro Val Glu Pro	
435	440	445
Asp Lys Val Glu Glu Ala Asn Lys Gly Glu Asn Thr	Ser Leu Leu His	
450	455	460
Pro Val Ser Leu His Gly Met Asp Asp Pro Glu Arg	Glu Val Leu Glu	
465	470	475
Trp Arg Phe Asp Ser His Leu Ala Phe His His Val	Ala Arg Glu Leu	
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His Pro Glu Tyr Phe Lys Asn Cys		
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<210> 7

<211> 1518

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of the p17/24opt/trNef insert
in p17/24opt/trNef1

<400> 7

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ctggggcaat tgcagccatc cctccagacc gggagtgaag agctgaggtc cttgtataaac 240
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gacactgggc atagcaacca ggtatcacag aactatccta ttgtccaaaa cattcaggcc 420
cagatgggtc atcaggccat cagccccgg acgctcaatg cctgggtgaa ggttgtcgaa 480
gagaaggcct tttctcctga ggttatcccc atgttctccg ctttgagtgaa gggggccact 540
cctcaggacc tcaataacaat gcttaatacc gtggggggcc atcaggccgc catgcaaatg 600
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ggcccaatcg cggccggaca gatgcgggag cctcgccgct ctgacattgc cggcaccacc 720
tctacactgc aagagcaaat cggatggatg accacaatac cttccatccc agttggagaa 780
atctataaac ggtggatcat tctcggtctc aataaaattg tttagaatgtt ctctccgaea 840

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 gccaccctgg aagagatgtat gacccgcctgt cagggagtag gccggaccggg acacaaagcc 1080
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 aaggcagctg tagatcttag ccacttttta aaagaaaagg ggggactgga agggctaatt 1200
 cactcccaa gaagacaaga tatccttgat ctgtggatct accacacaca aggtacttc 1260
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 tgcataaagg tagtaccagt tgagccagat aagtagaaag aggccaataa aggagagaac 1380
 accagcttgt tacaccctgt gacccctgcat gggatggatg acccggagag agaagtgtta 1440
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 tacttcaaga actgctga 1518

<210> 8

<211> 505

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acid sequence of the p17/24opt/trNef insert
in p17/24opt/trNef1

<400> 8

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Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys	Lys	Tyr	Lys	Lys		
									20		25				30
His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu	Arg	Phe	Ala	Val	Asn	Pro
									35		40				45
Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg	Gln	Ile	Leu	Gly	Gln	Leu
									50		55				60
Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu	Leu	Arg	Ser	Leu	Tyr	Asn
									65		70				80
Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln	Arg	Ile	Glu	Ile	Lys	Asp
									85		90				95
Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu	Gln	Asn	Lys	Ser	Lys	
									100		105				110
Lys	Lys	Ala	Gln	Gln	Ala	Ala	Asp	Thr	Gly	His	Ser	Asn	Gln	Val	
									115		120				125
Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile	Gln	Gly	Gln	Met	Val	His
									130		135				140
Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val	Val	Glu
									145		150				160
Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Ser	Ala	Leu	Ser
									165		170				175
Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr	Val	Gly
									180		185				190
Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys	Glu	Thr	Ile	Asn	Glu	Glu
									195		200				205
Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val	His	Ala	Gly	Pro	Ile	Ala
									210		215				220
Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser	Asp	Ile	Ala	Gly	Thr	Thr
									225		230				240
Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met	Thr	Asn	Asn	Pro	Pro	Ile
									245		250				255
Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile	Ile	Leu	Gly	Leu	Asn	Lys
									260		265				270
Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile	Leu	Asp	Ile	Arg	Gln	Gly
									275		280				285

Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
 290 295 300
 Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr
 305 310 315 320
 Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala
 325 330 335
 Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly
 340 345 350
 Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Met Val Gly Phe Pro
 355 360 365
 Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr Tyr Lys Ala Ala Val
 370 375 380
 Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly Leu Glu Gly Leu Ile
 385 390 395 400
 His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu Trp Ile Tyr His Thr
 405 410 415
 Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr Pro Gly Pro Gly Val
 420 425 430
 Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys Leu Val Pro Val Glu
 435 440 445
 Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu Asn Thr Ser Leu Leu
 450 455 460
 His Pro Val Ser Leu His Gly Met Asp Asp Pro Glu Arg Glu Val Leu
 465 470 475 480
 Glu Trp Arg Phe Asp Ser His Leu Ala Phe His His Val Ala Arg Glu
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 Leu His Pro Glu Tyr Phe Lys Asn Cys
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<210> 9

<211> 1689

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of RT insert of p7077-RT3

<400> 9

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 accgagatgg agaaaagaggg caagatcagc aagatcgggc ctgagaaccc atacaacacc 180
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 ggcttgaaga agaagaagag cgtgaccgtg ctggacgtgg gcgacgtta cttcagcgtc 360
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 acccctggca tcagatatca gtacaacgtc ctcccccagg gctggaaagg ctctccggcc 480
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<210> 10

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acid sequence of RT insert of p7077-RT3

<400> 10

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										25				30	
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						50				55				60	
Ile	Lys	Lys	Ile	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	Arg
						65				70				75	
Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	Ile
						85				90				95	
Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Lys	Ser	Val	Thr	Val	Leu	Asp	
						100				105				110	
Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Glu	Asp	Phe	Arg	Lys
						115				120				125	
Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly	Ile
						130				135				140	
Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	Ala
						145				150				155	
Ile	Phe	Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	Gln
						165				170				175	
Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	Gly
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Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Ile	Glu	Glu	Leu	Arg
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Gln	His	Leu	Leu	Arg	Trp	Gly	Leu	Thr	Thr	Pro	Asp	Lys	Lys	His	Gln
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Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	Lys
						225				230				235	
Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr	Val
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Asn	Asp	Ile	Gln	Lys	Leu	Val	Gly	Lys	Leu	Asn	Trp	Ala	Ser	Gln	Ile
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Tyr	Pro	Gly	Ile	Lys	Val	Arg	Gln	Leu	Cys	Lys	Leu	Leu	Arg	Gly	Thr
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Lys	Ala	Leu	Thr	Glu	Val	Ile	Pro	Leu	Thr	Glu	Glu	Ala	Glu	Leu	Glu
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Leu	Ala	Glu	Asn	Arg	Glu	Ile	Leu	Lys	Glu	Pro	Val	His	Gly	Val	Tyr
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															320

Tyr Asp Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln
 325 330 335
 Gly Gln Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys
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 Thr Gly Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys
 355 360 365
 Gln Leu Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile
 370 375 380
 Trp Gly Lys Thr Pro Lys Phe Lys Leu Pro Ile Gln Lys Glu Thr Trp
 385 390 395 400
 Glu Thr Trp Trp Thr Glu Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp
 405 410 415
 Glu Phe Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu
 420 425 430
 Lys Glu Pro Ile Val Gly Ala Glu Thr Phe Tyr Val Asp Gly Ala Ala
 435 440 445
 Asn Arg Glu Thr Lys Leu Gly Lys Ala Gly Tyr Val Thr Asn Arg Gly
 450 455 460
 Arg Gln Lys Val Val Thr Leu Thr Asp Thr Thr Asn Gln Lys Thr Glu
 465 470 475 480
 Leu Gln Ala Ile Tyr Leu Ala Leu Gln Asp Ser Gly Leu Glu Val Asn
 485 490 495
 Ile Val Thr Asp Ser Gln Tyr Ala Leu Gly Ile Ile Gln Ala Gln Pro
 500 505 510
 Asp Gln Ser Glu Ser Glu Leu Val Asn Gln Ile Ile Glu Gln Leu Ile
 515 520 525
 Lys Lys Glu Lys Val Tyr Leu Ala Trp Val Pro Ala His Lys Gly Ile
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 Val Leu

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 accgagatgg agaaagaggg caagatcagc aagatcgggc ctgagaaccc atacaacacc 180
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<211> 561

<212>. PRT

<213> Artificial Sequence

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<223> amino acid sequence of the coding insert in
p73i-RT3

<400> 12

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Ala Leu Thr Glu Val Ile Pro Leu Thr Glu Glu Ala Glu Leu Glu Leu
290 295 300
Ala Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr Tyr
305 310 315 320
Asp Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln Gly
325 330 335
Gln Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr
340 345 350
Gly Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys Gln
355 360 365
Leu Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile Trp
370 375 380
Gly Lys Thr Pro Lys Phe Lys Leu Pro Ile Gln Lys Glu Thr Trp Glu
385 390 395 400
Thr Trp Trp Thr Glu Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp Glu
405 410 415
Phe Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu Lys
420 425 430
Glu Pro Ile Val Gly Ala Glu Thr Phe Tyr Val Asp Gly Ala Ala Asn
435 440 445
Arg Glu Thr Lys Leu Gly Lys Ala Gly Tyr Val Thr Asn Arg Gly Arg
450 455 460
Gln Lys Val Val Thr Leu Thr Asp Thr Thr Asn Gln Lys Thr Glu Leu
465 470 475 480
Gln Ala Ile Tyr Leu Ala Leu Gln Asp Ser Gly Leu Glu Val Asn Ile
485 490 495
Val Thr Asp Ser Gln Tyr Ala Leu Gly Ile Ile Gln Ala Gln Pro Asp
500 505 510
Gln Ser Glu Ser Glu Leu Val Asn Gln Ile Ile Glu Gln Leu Ile Lys
515 520 525
Lys Glu Lys Val Tyr Leu Ala Trp Val Pro Ala His Lys Gly Ile Gly
530 535 540
Gly Asn Glu Gln Val Asp Lys Leu Val Ser Ala Gly Ile Arg Lys Val
545 550 555 560
Leu

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